

## SEQUENCE LISTING

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40

<110> Briggs, Clark A.  
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Abbott Laboratories

<120> A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE  
RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF

<130> 6017.US.01

<140> 08/771,737  
<141> 1996-12-20

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tct ctc ctg cac gtg tcc ctg caa ggc gag ttc cag agg aag ctt tac 98  
Ser Leu Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr  
15 20 25 30

aag gag ctg gtc aag aac tac aat ccc ttg gag agg ccc gtg gcc aat 146  
Lys Glu Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn  
35 40 45

gac tcg caa cca ctc acc gtc tac ttc tcc ctg agc ctc ctg cag atc 194  
Asp Ser Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Gln Ile  
50 55 60

atg gac gtg gat gag aag aac caa gtt tta acc acc aac att tgg ctg 242  
Met Asp Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu  
65 70 75

caa atg tct tgg aca gat cac tat tta cag tgg aat gtg tca gaa tat 290  
Gln Met Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr

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cca ggg gtg aag act gtt cgt ttc cca gat ggc cag att tgg aaa cca Pro Gly Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro	95	100	105	338
95	100	105	110	
gac att ctt ctc tat aac agt gct gat gag cgc ttt gac gcc aca ttc Asp Ile Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe	115	120	125	386
115	120	125		
cac act aac gtg ttg gtg aat tct tct ggg cat tgc cag tac ctg cct His Thr Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro	130	135	140	434
130	135	140		
cca ggc ata ttc aag agt tcc tgc tac atc gat gta cgc tgg ttt ccc Pro Gly Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro	145	150	155	482
145	150	155		
ttt gat gtg cag cac tgc aaa ctg aag ttt ggg tcc tgg tct tac gga Phe Asp Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly	160	165	170	530
160	165	170		
ggc tgg tcc ttg gat ctg cag atg cag gag gca gat atc agt ggc tat Gly Trp Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr	175	180	185	578
175	180	185	190	
atc ccc aat gga gaa tgg gac cta gtg gga atc ccc ggc aag agg agt Ile Pro Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser	195	200	205	626
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gaa agg ttc tat gag tgc tgc aaa gag ccc tac ccc gat gtc acc ttc Glu Arg Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe	210	215	220	674
210	215	220		
aca gtg acc atg cgc cgc agg aca ctc tac tat ggc ctc aac ctg ctg Thr Val Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu	225	230	235	722
225	230	235		
atc ccc tgt gtg ctc atc tcc gcc ctc gcc ctg ctg gtg ttc ctg ctt Ile Pro Cys Val Leu Ile Ser Ala Leu Ala Leu Val Phe Leu Leu	240	245	250	770
240	245	250		
cct gca gat tcc ggg gag aag att tcc ctg ggg ata aca gtc tta ctc Pro Ala Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu	255	260	265	818
255	260	265	270	
tct ctt acc acc ttc atg ctg ctc gtg gct gag atc atg ccc gca aca Ser Leu Thr Thr Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr	275	280	285	866
275	280	285		
tcc gat tcg gta cca ttg ata gcc cag tac ttc gcc agc acc atg atc Ser Asp Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile	290	295	300	914
290	295	300		
atc gtg ggc ctc tcg gtg gtg acg gtg atc gtg ctg cag tac cac Ile Val Gly Leu Ser Val Val Val Thr Val Ile Val Leu Gln Tyr His	305	310	315	962
305	310	315		

*375*  
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cac cac gac ccc gac ggc aag atg ccc aag tgg acc aga gtc atc 1010  
His His Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Val Ile  
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ctt ctg aac tgg tgc gcg tgg ttc ctg cga atg aag agg ccc ggg gag 1058  
Leu Leu Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu  
335 340 345 350

gac aag gtg cgc ccg gcc tgc cag cac aag cag cgg cgc tgc agc ctg 1106  
Asp Lys Val Arg Pro Ala Cys Gln His Lys Gln Arg Arg Cys Ser Leu  
355 360 365

gcc agt gtg gag atg agc gcc gtg gcg ccg ccc gcc agc aac ggg 1154  
Ala Ser Val Glu Met Ser Ala Val Ala Pro Pro Pro Ala Ser Asn Gly  
370 375 380

aac ctg ctg tac atc ggc ttc cgc ggc ctg gac ggc gtg cac tgt gtc 1202  
Asn Leu Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val  
385 390 395

ccg acc ccc gac tct ggg gta gtg tgt ggc cgc atg gcc tgc tcc ccc 1250  
Pro Thr Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro  
400 405 410

acg cac gat gag cac ctc ctg cac ggc ggg caa ccc ccc gag ggg gac 1298  
Thr His Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp  
415 420 425 430

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Pro Asp Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg  
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Phe Arg Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe  
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gcc gcc tgt gtg gtg gac cgc ctg tgc ctc atg gcc ttc tcg gtc ttc 1442  
Ala Ala Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe  
465 470 475

acc atc atc tgc acc atc ggc atc ctg atg tcg gct ccc aac ttc gtg 1490  
Thr Ile Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val  
480 485 490

gag gcc gtg tcc aaa gac ttt gcg taaccacgcc tggttctgta catgtggaaa 1544  
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				20				25					30			
Leu	Val	Lys	Asn	Tyr	Asn	Pro	Leu	Glu	Arg	Pro	Val	Ala	Asn	Asp	Ser	
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Gln	Pro	Leu	Thr	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Leu	Gln	Ile	Met	Asp	
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Val	Asp	Glu	Lys	Asn	Gln	Val	Leu	Thr	Thr	Asn	Ile	Trp	Leu	Gln	Met	
				65				70			75		80			
Ser	Trp	Thr	Asp	His	Tyr	Leu	Gln	Trp	Asn	Val	Ser	Glu	Tyr	Pro	Gly	
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Val	Lys	Thr	Val	Arg	Phe	Pro	Asp	Gly	Gln	Ile	Trp	Lys	Pro	Asp	Ile	
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Leu	Leu	Tyr	Asn	Ser	Ala	Asp	Glu	Arg	Phe	Asp	Ala	Thr	Phe	His	Thr	
				115				120			125					
Asn	Val	Leu	Val	Asn	Ser	Ser	Gly	His	Cys	Gln	Tyr	Leu	Pro	Pro	Gly	
				130				135			140					
Ile	Phe	Lys	Ser	Ser	Cys	Tyr	Ile	Asp	Val	Arg	Trp	Phe	Pro	Phe	Asp	
				145				150			155		160			
Val	Gln	His	Cys	Lys	Leu	Lys	Phe	Gly	Ser	Trp	Ser	Tyr	Gly	Gly	Trp	
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Ser	Leu	Asp	Leu	Gln	Met	Gln	Glu	Ala	Asp	Ile	Ser	Gly	Tyr	Ile	Pro	
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Asn	Gly	Glu	Trp	Asp	Leu	Val	Gly	Ile	Pro	Gly	Lys	Arg	Ser	Glu	Arg	
				195				200			205					
Phe	Tyr	Glu	Cys	Cys	Lys	Glu	Pro	Tyr	Pro	Asp	Val	Thr	Phe	Thr	Val	
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Thr	Met	Arg	Arg	Arg	Arg	Thr	Leu	Tyr	Tyr	Gly	Leu	Asn	Leu	Leu	Ile	Pro
				225				230			235		240			
Cys	Val	Leu	Ile	Ser	Ala	Leu	Ala	Leu	Leu	Val	Phe	Leu	Leu	Pro	Ala	
					245				250			255				
Asp	Ser	Gly	Glu	Lys	Ile	Ser	Leu	Gly	Ile	Thr	Val	Leu	Leu	Ser	Leu	
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Thr	Thr	Phe	Met	Leu	Leu	Val	Ala	Glu	Ile	Met	Pro	Ala	Thr	Ser	Asp	
				275				280			285					
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					325				330			335				
Asn	Trp	Cys	Ala	Trp	Phe	Leu	Arg	Met	Lys	Arg	Pro	Gly	Glu	Asp	Lys	
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Val	Arg	Pro	Ala	Cys	Gln	His	Lys	Gln	Arg	Arg	Cys	Ser	Leu	Ala	Ser	
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Val	Glu	Met	Ser	Ala	Val	Ala	Pro	Pro	Ala	Ser	Asn	Gly	Asn	Leu		
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Leu	Tyr	Ile	Gly	Phe	Arg	Gly	Leu	Asp	Gly	Val	His	Cys	Val	Pro	Thr	
				385				390			395		400			
Pro	Asp	Ser	Gly	Val	Val	Cys	Gly	Arg	Met	Ala	Cys	Ser	Pro	Thr	His	
					405				410			415				
Asp	Glu	His	Leu	Leu	His	Gly	Gly	Gln	Pro	Pro	Glu	Gly	Asp	Pro	Asp	
				420				425			430					
Leu	Ala	Lys	Ile	Leu	Glu	Glu	Val	Arg	Tyr	Ile	Ala	Asn	Arg	Phe	Arg	
				435				440			445					
Cys	Gln	Asp	Glu	Ser	Glu	Ala	Val	Cys	Ser	Glu	Trp	Lys	Phe	Ala	Ala	

515 44

450	455	460	
Cys Val Val Asp Arg Leu	Cys Leu Met Ala Phe Ser Val Phe Thr Ile		
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Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val Glu Ala			
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Val Ser Lys Asp Phe Ala	.		
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